DSC680 - Project 2

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Overview

- Introduction of Problem
- Data Source
- Data Exploration
- Machine Learning Models
- Conclusion

Introduction of Problem

- Diseases spread from animals to humans (Zoonotic Diseases)
- Important to understand animal diseases
- Data Science can help to find answers to possible questions
    - What factors can help predict presence of blood pathogens?
    - Are blood samples required?
    - Can a location of an outbreak be identified?

Data Source

- Data collected on Alaskan crows from 2007-2008
- Alaskan Science Center
- Concern of growth in beak deformities
    - Avian Keratin Disorder (AKD)

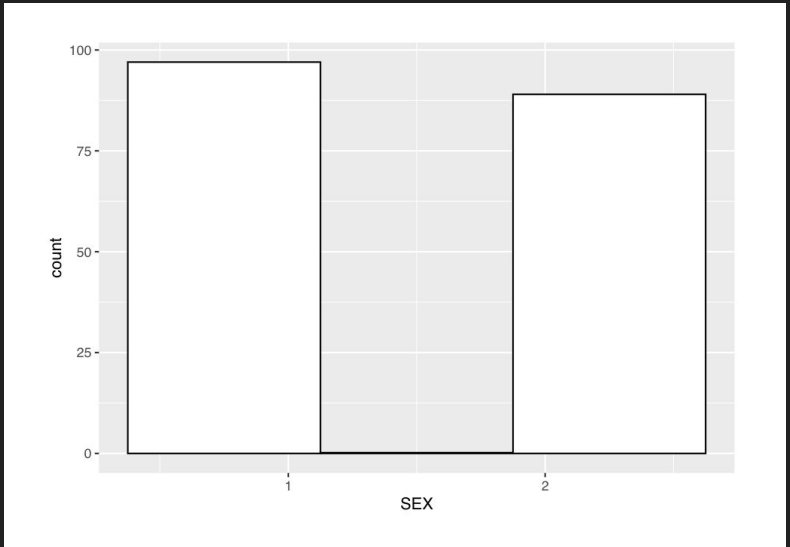
Data Source

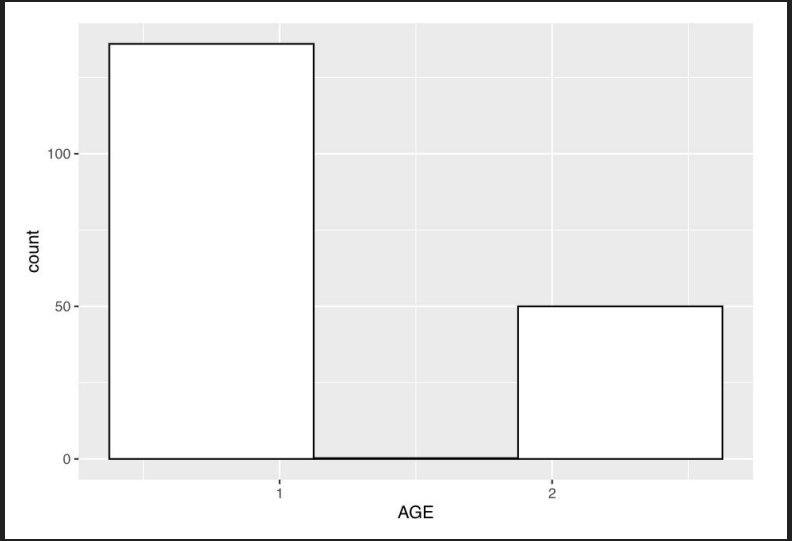
- Samples of over 180 crows
- Biological data and blood samples
- Studied for presence of three blood pathogens
  - Leucocytozoon parasite infection (LEUC)
  - Haemoproteus parasite infection (HAEM)
  - Plasmodium parasite infection (PLAS)

Data Exploration

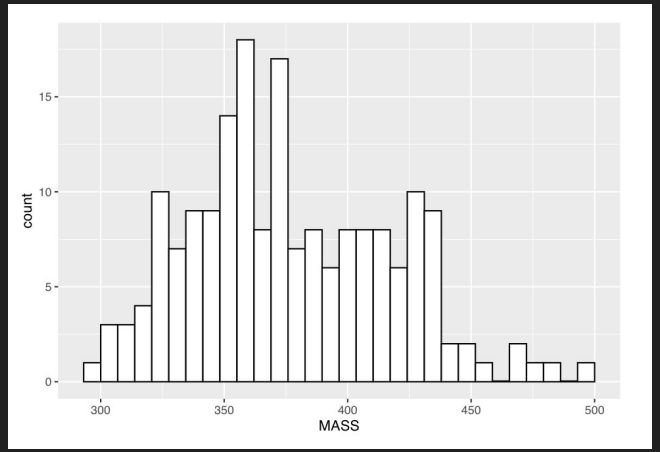
- All functions, graphs, and visuals created in R
- Six locations
  - One-hot encoding used for the machine learning algorithms
- Two tests for each pathogen
  - First test result was used for the majority of analysis

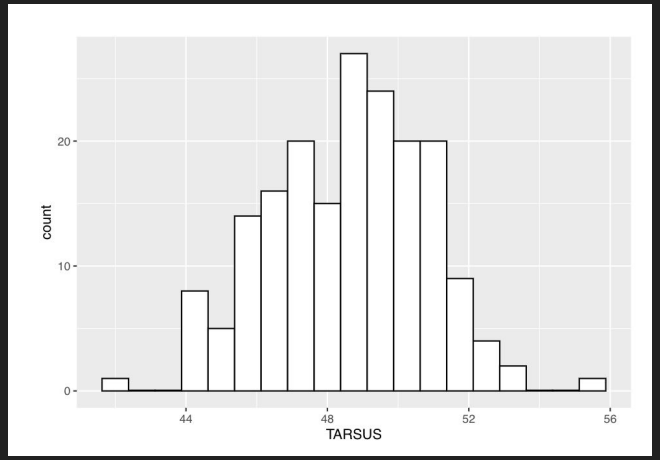
Data Exploration



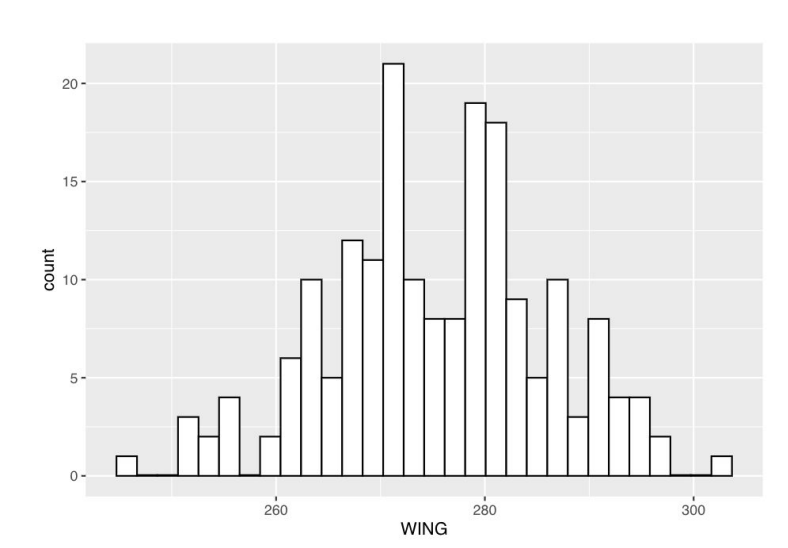


Data Exploration

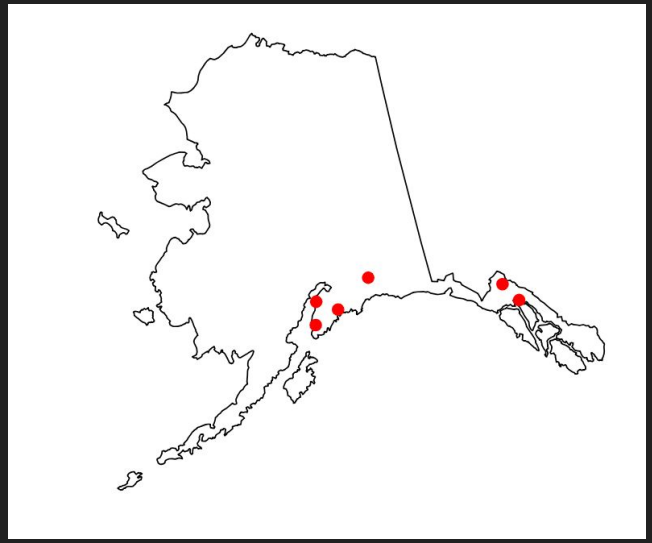


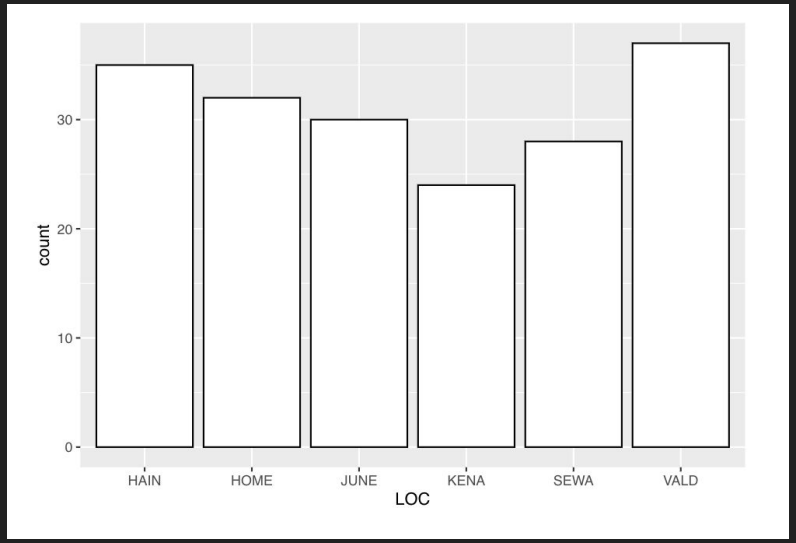


Data Exploration



Data Exploration





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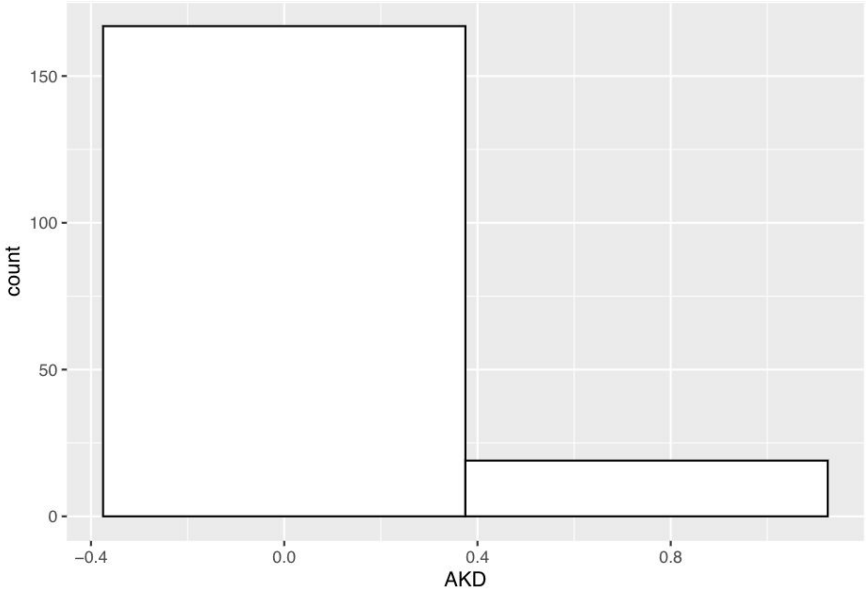
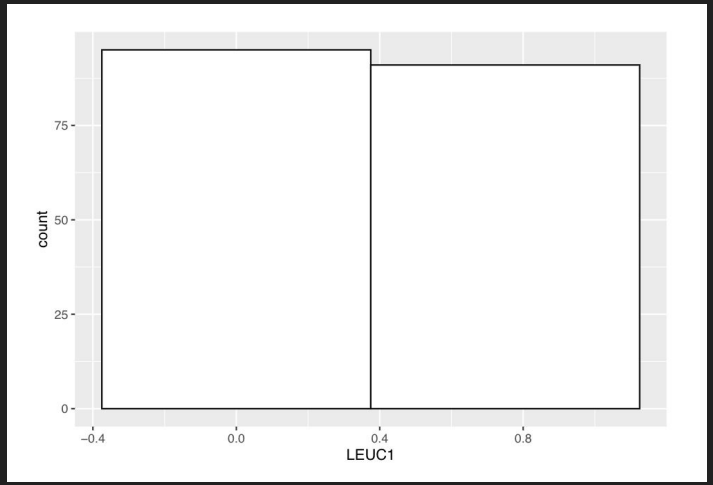
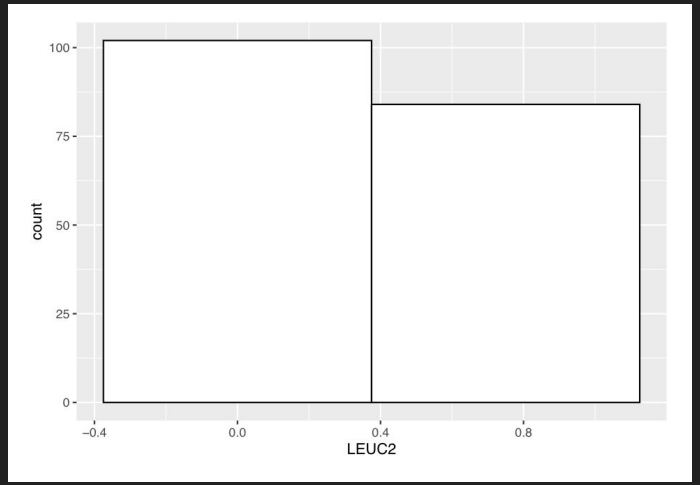
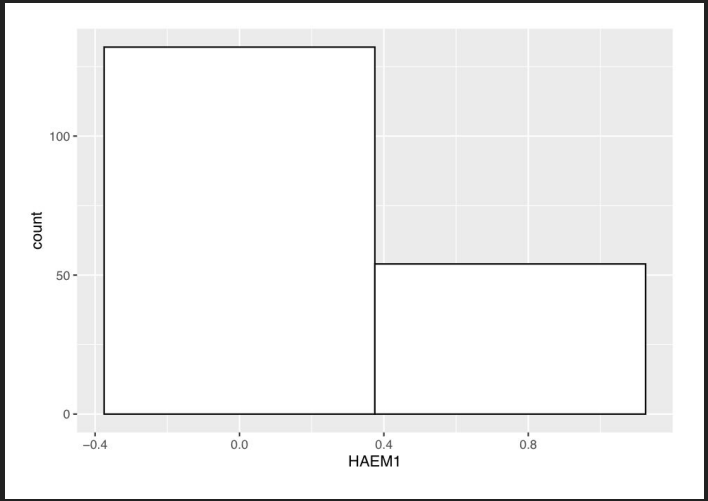


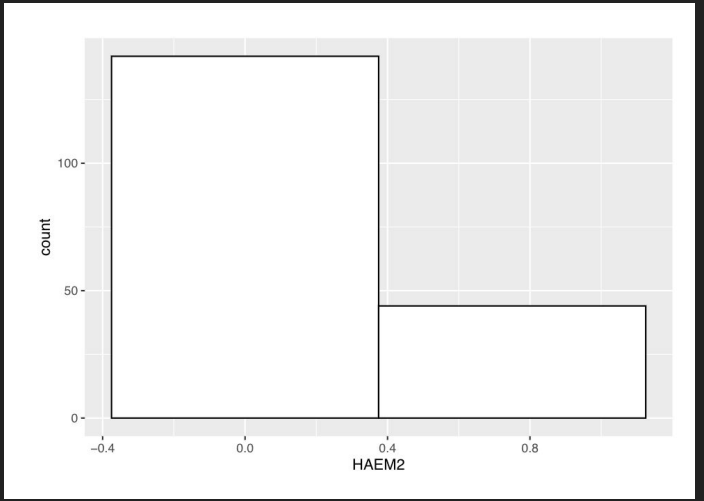
Data Exploration





Data Exploration





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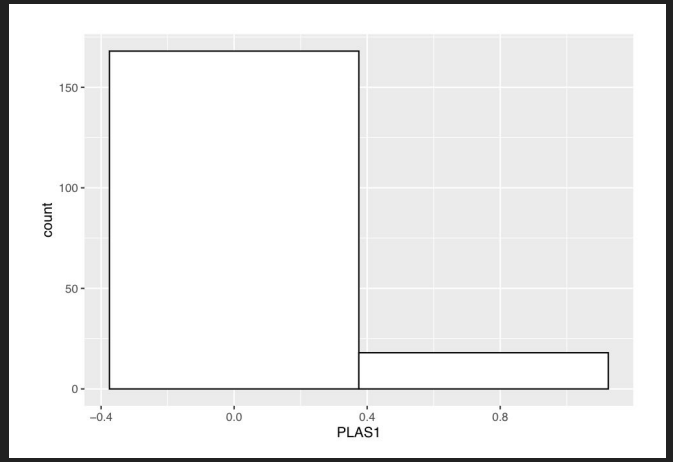
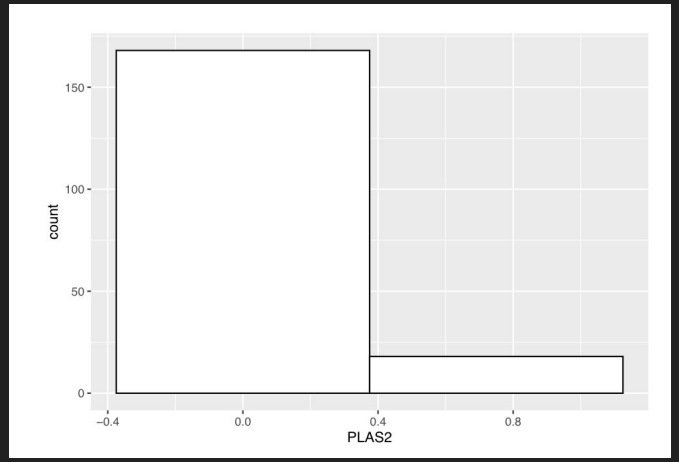
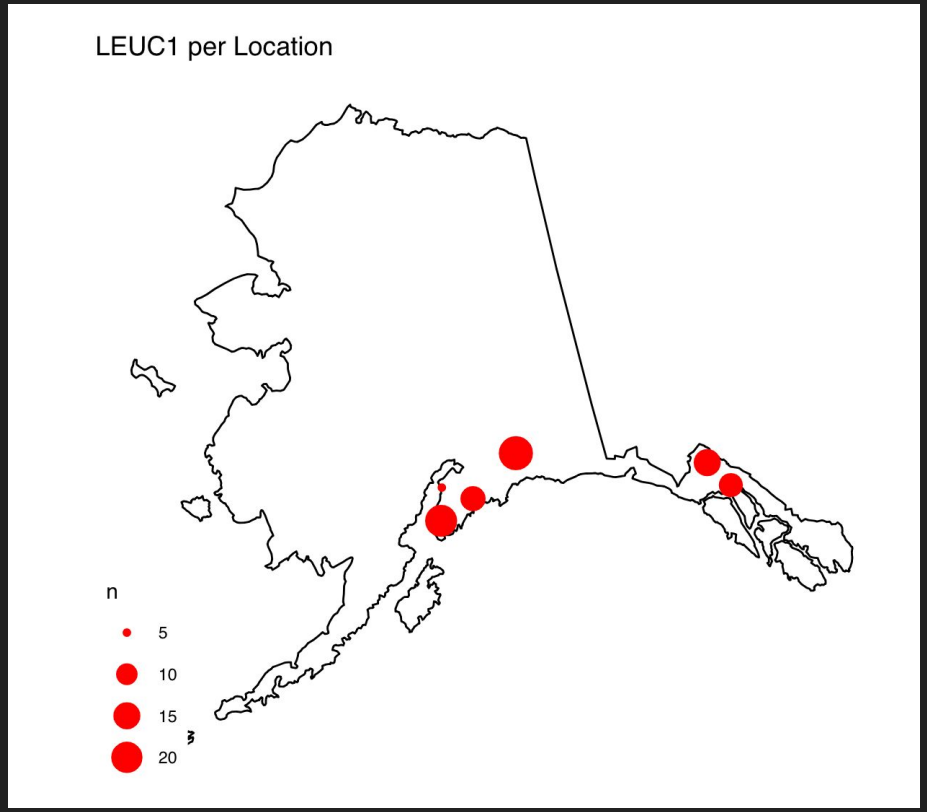
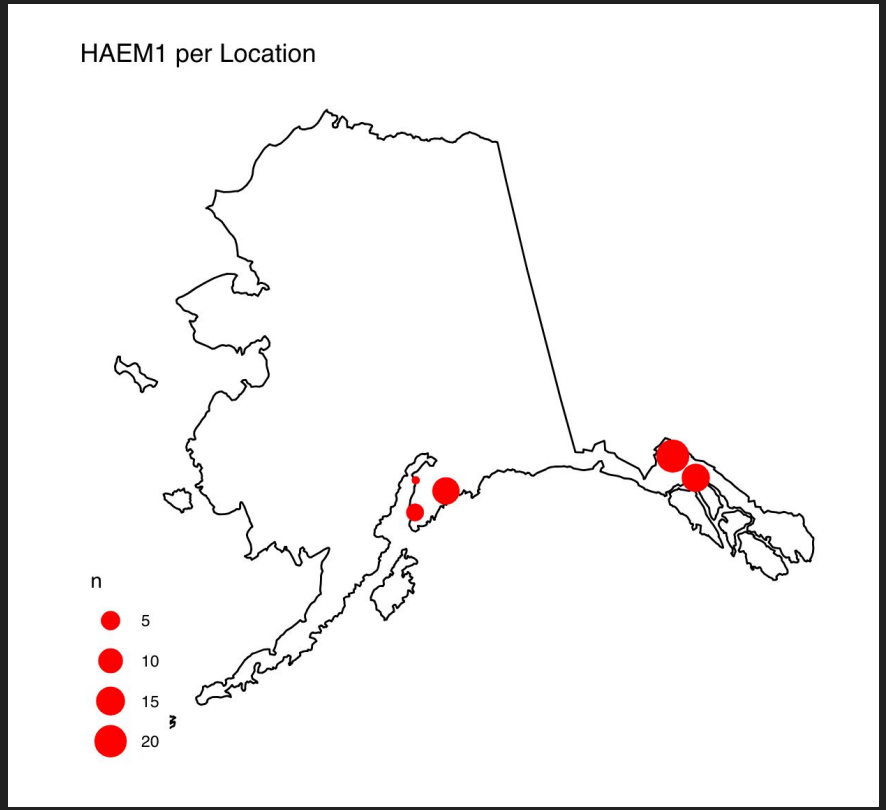




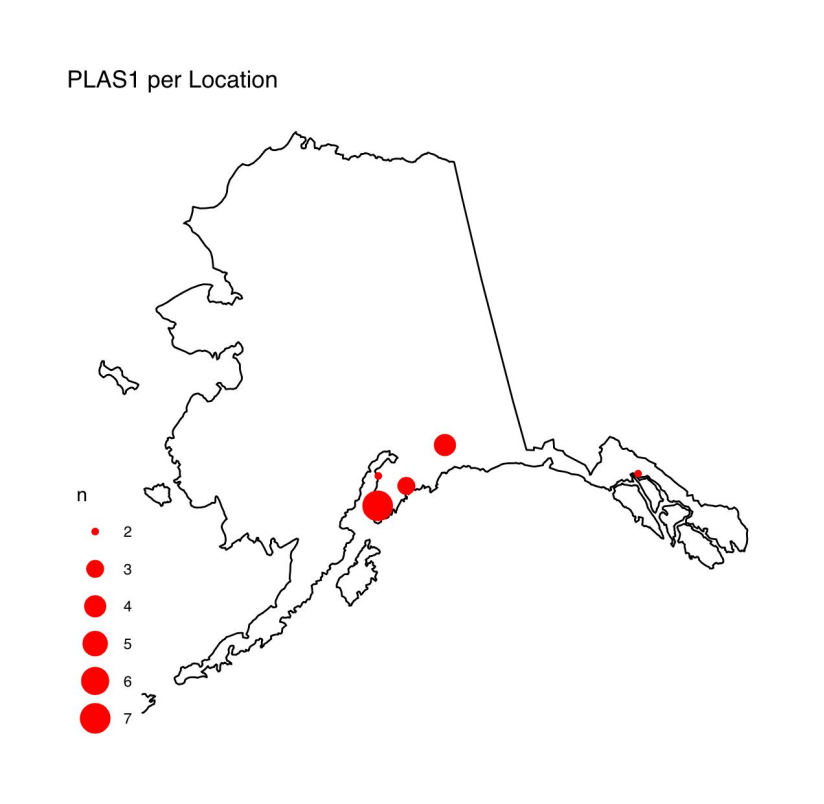
Data Exploration



Data Exploration



Data Exploration



Machine Learning Models

- Target Variables
  - AKD
  - LEUC1
  - HAEM1
  - PLAS1
- No significant covariance or correlation between target variables and any feature variables
- Linear Regression Model found no significant relationships

Machine Learning Models

- 3 Algorithms Used
  - Logistic Regression
  - Decision Tree
  - Naive Bayes
- Target variables are binary

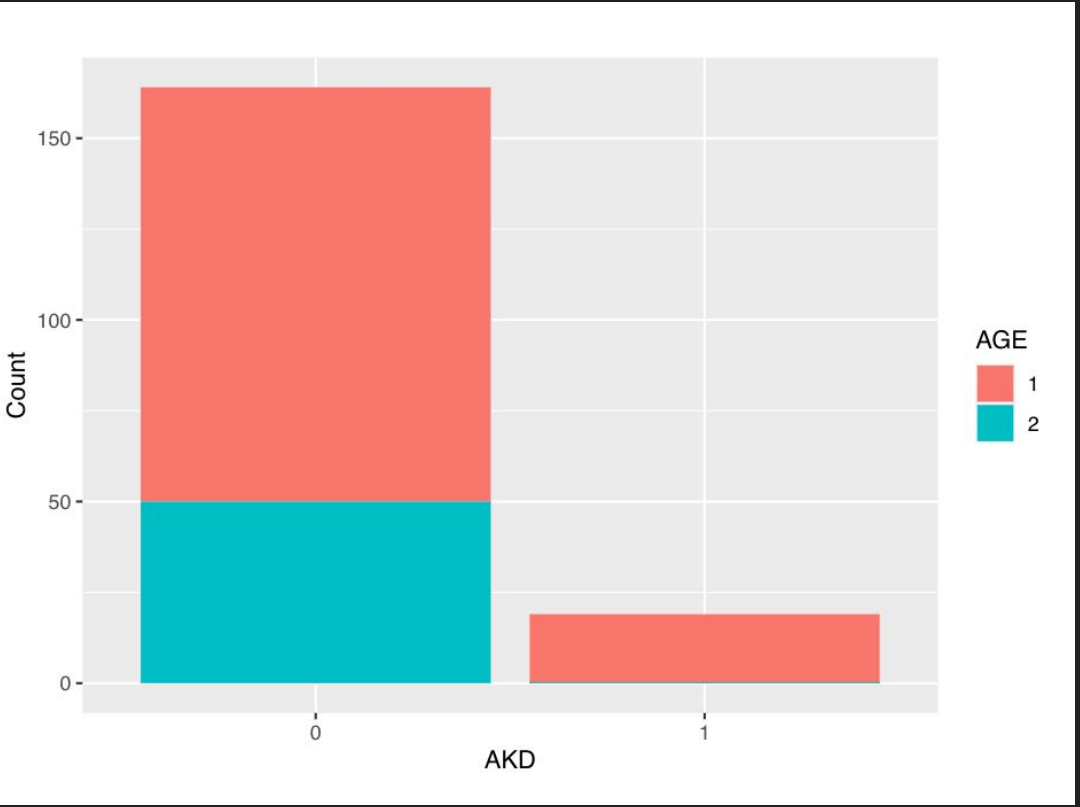
Logistic Regression - AKD

```
##                    2.5 %       97.5 %
## (Intercept) -2634.1900120 2.703235e+03
## SEX            -1.7216634 6.205950e-01
## AGE         -2687.5585861 2.649684e+03
## TARSUS         -0.5595384 1.466764e-01
## WING           -0.1411362 3.639016e-02
## MASS           -0.0105768 4.295700e-02
## LEUC1          -1.4942911 9.954247e-01
## HAEM1          -0.4354375 2.801334e+00
## PLAS1          -1.1808293 2.272975e+00
## LOC.SEWA        0.3159412 5.206111e+00
## LOC.KENA        0.4843588 5.526163e+00
## LOC.VALD       -0.9485564 3.915921e+00
## LOC.HAIN       -3.1540757 2.962598e+00
## LOC.JUNE       -1.3598649 3.762584e+00
## LOC.HOME               NA          NA
```

	FALSE	TRUE
0	121	2
1	12	2

Accuracy = 89.78%

Logistic Regression - AKD



Logistic Regression - LEUC1

```
##                    2.5 %       97.5 %
## (Intercept) -17.71263917  5.909124006
## SEX          -1.31020091  0.040505299
## AGE          -0.64902989  0.988229952
## TARSUS       -0.16748996  0.251269057
## WING         -0.01898793  0.079701079
## MASS         -0.02030441  0.004506129
## AKD          -1.39307227  0.850198909
## HAEM1        -0.25512635  1.438850338
## PLAS1        -1.41951384  0.862883216
## LOC.SEWA     -2.33247532  0.224501978
## LOC.KENA     -3.49483430 -0.744937835
## LOC.VALD     -1.24105373  0.962057262
## LOC.HAIN     -2.60165698 -0.162969019
## LOC.JUNE     -2.73548874 -0.310925938
## LOC.HOME              NA           NA
```

	FALSE	TRUE
0	49	21
1	21	47

Accuracy = 69.57%

Logistic Regression - HAEM1

```
##                    2.5 %       97.5 %
## (Intercept) -2.555382e+01 6.897946e+00
## SEX         -9.989220e-01 7.764953e-01
## AGE          2.875900e-01 2.583641e+00
## TARSUS      -1.322820e-01 4.189151e-01
## WING        -5.266542e-02 7.420183e-02
## MASS        -2.597683e-02 5.088832e-03
## LEUC1       -2.017605e-01 1.558561e+00
## AKD         -8.411244e-01 2.107398e+00
## PLAS1       -4.370732e+03 4.334582e+03
## LOC.SEWA    -5.049756e-01 2.711085e+00
## LOC.KENA    -4.645821e+00 2.663481e-01
## LOC.VALD    -3.216350e+03 3.179455e+03
## LOC.HAIN     3.676849e-01 3.202834e+00
## LOC.JUNE    -1.759188e-01 2.749479e+00
## LOC.HOME              NA           NA
```

	FALSE	TRUE
0	90	8
1	12	28

Accuracy = 85.5%

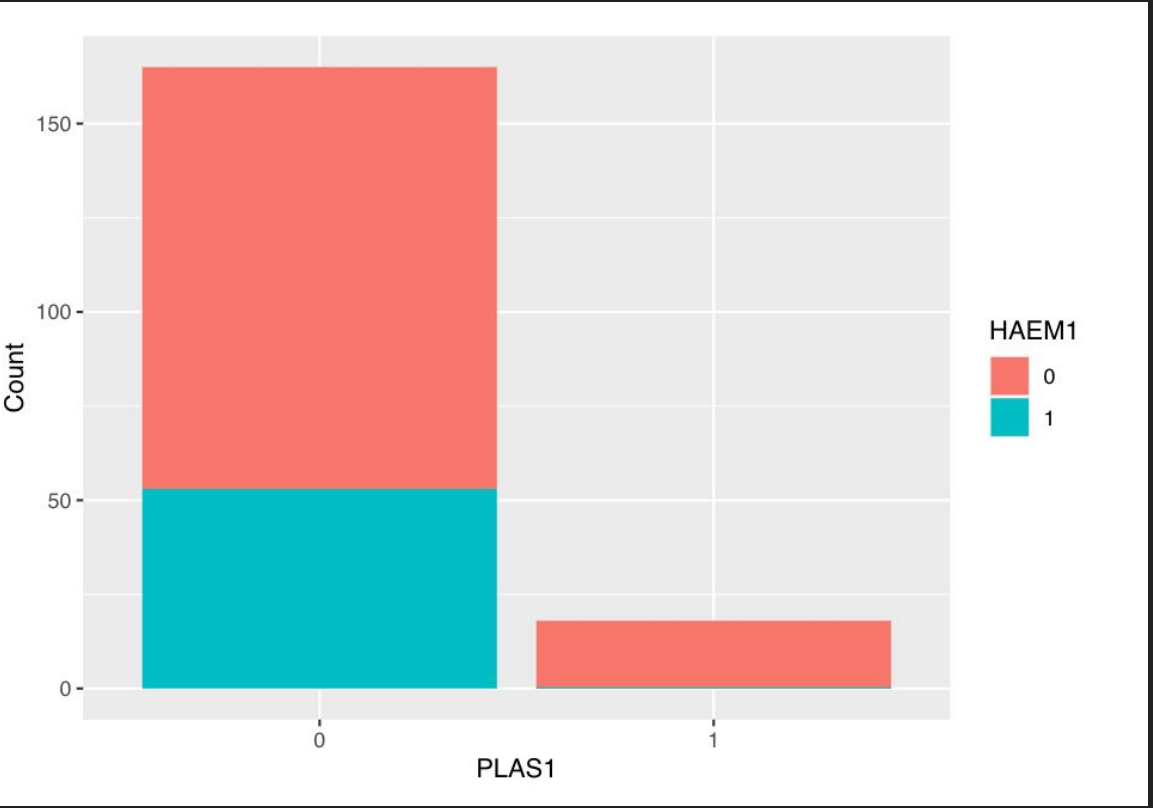
Logistic Regression - PLAS1

```
##                    2.5 %        97.5 %
## (Intercept) -4.024072e+01  3.899895e+00
## SEX         -1.182815e+00  1.132212e+00
## AGE         -1.785850e+00  1.738433e+00
## TARSUS      -5.059899e-01  2.209062e-01
## WING         2.125323e-02  2.226448e-01
## MASS        -5.219369e-02 -1.072603e-03
## LEUC1       -1.421506e+00  9.861846e-01
## HAEM1       -4.066102e+03  4.028546e+03
## AKD         -7.635654e-01  2.683554e+00
## LOC.SEWA    -1.478637e+00  2.524080e+00
## LOC.KENA    -3.550206e+00  5.054281e-01
## LOC.VALD    -2.356527e+00  5.392387e-01
## LOC.HAIN    -4.900745e+03  4.865228e+03
## LOC.JUNE    -2.369083e+00  1.309431e+00
## LOC.HOME              NA            NA
```

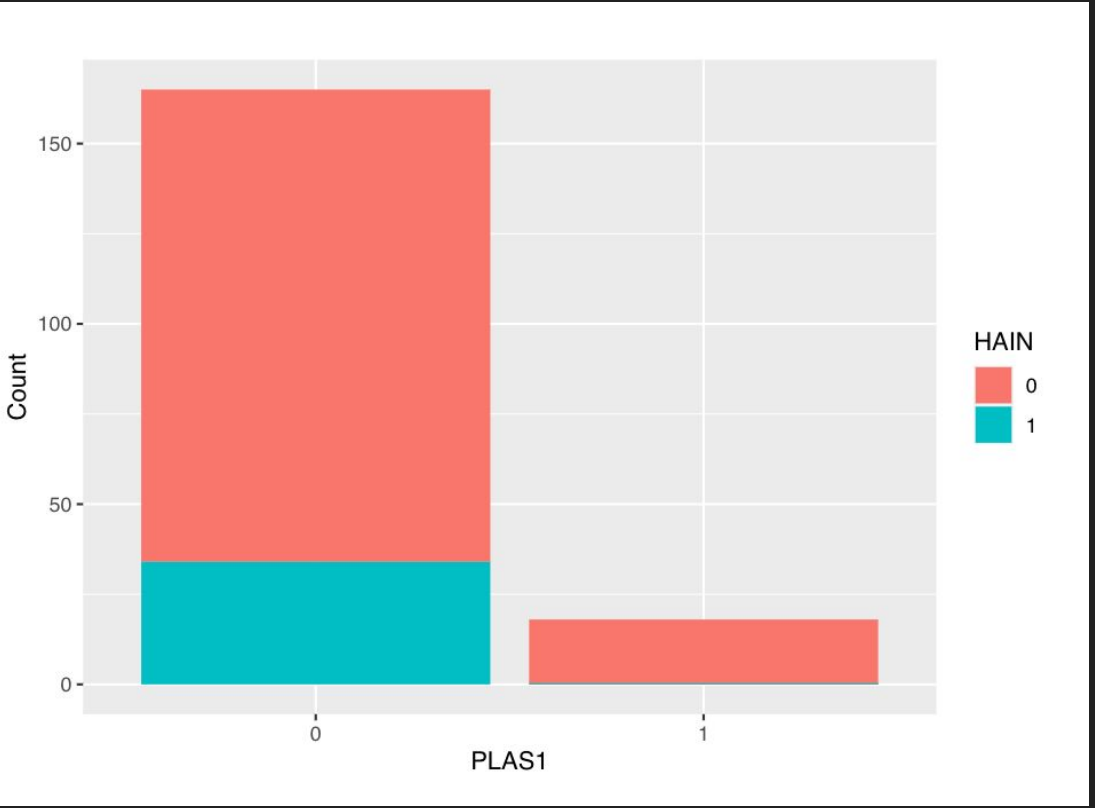
	FALSE	TRUE
0	123	1
1	10	4

Accuracy = 92%

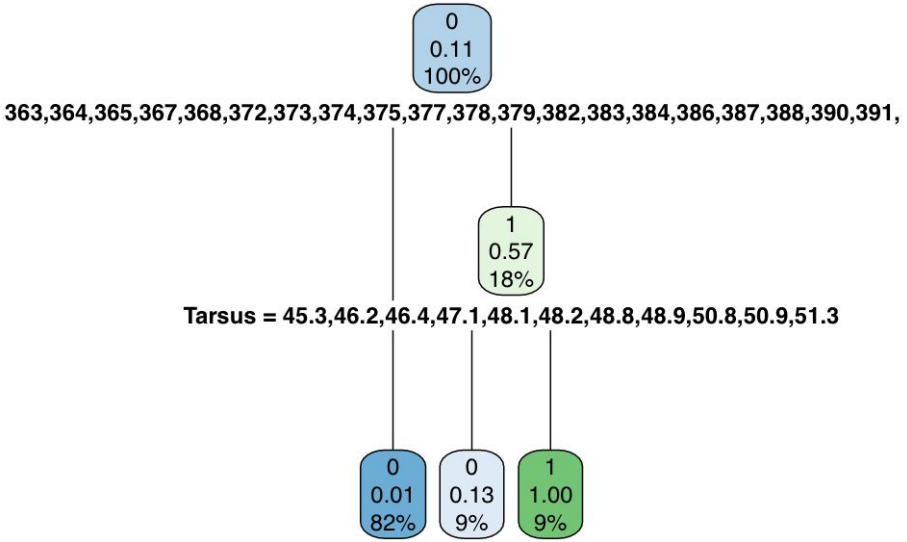
Logistic Regression - PLAS1



Logistic Regression - PLAS1



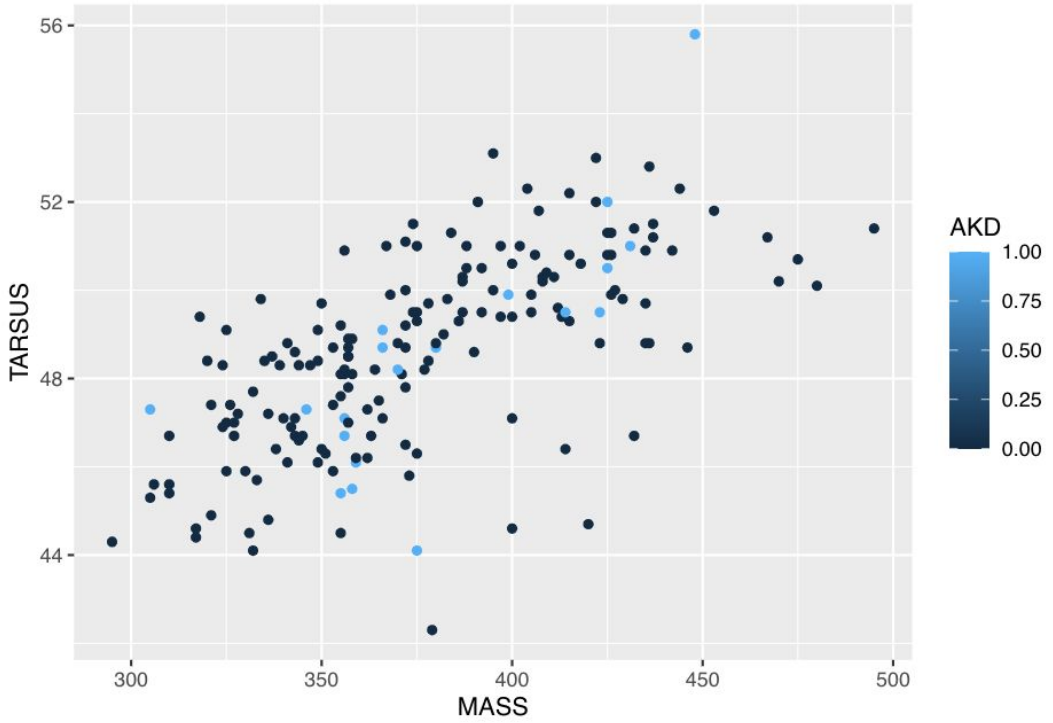
Decision Tree - AKD




```
p <- predict(dtm, data_test, type="class")
confMat <- table(data_test$AKD,p)
accuracy <- sum(diag(confMat))/sum(confMat)
return (accuracy*100)
```

```
## [1] 94.73684
```

Decision Tree - AKD



Decision Tree - Pathogens

- LEUC1 - 47.37%
- HAEM1 - 63.16%
- PLAS1 - 73.68%

Naive Bayes - AKD

```
##
## p2    0  1
##   0 28  4
##   1  0  0
```

```
## [1] 87.5
```

Naive Bayes - LEUC1

```
#
# p2  0 1
#   0 8 8
#   1 8 8
```

```
## [1] 50
```

Naive Bayes - HAEM1

```
p2   0  1
  0 16  4
  1  4  8
```

```
## [1] 75
```

Naive Bayes - PLAS1

p2	0	1
0	25	5
1	2	0

```
[1] 78.125
```

Machine Learning Models

	Target Variable			
Algorithm	**AKD**	**LEUC1**	**HAEM1**	**PLAS1**
Logistic Regression	89.78%	69.57%	85.50%	92%
Decision Tree	94.70%	47.37%	63.16%	73.68%
Naive Bayes	87.50%	50%	75%	78.13%

Conclusion

- AKD has potential to be predicted reliably
  - Age, mass, tarsus
- Logistic Regression held potentially strong results
  - AKD
  - PLAS1
  - HAEM1